

Copyright (c) 1993 - 2004 Compugen Ltd.
GenCore version 5.1.6

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model
Run on: May 15, 2004, 04:52:59 ; Search time 8109 Seconds
(without alignments)
11037.534 Million cell updates/sec

Title: US-10-015-387A-219
Perfect score: 2065
Sequence: 1 gtaataatgtgggtttgtatg.....attataatatgttaaaaaaaaaa 2065

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 347072 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : GenEmbl:
 1: 9b_ba: *
 2: 9b_htg: *
 3: 9b_in: *
 4: 9b_om: *
 5: 9b_ov: *
 6: 9b_pat: *
 7: 9b_ph: *
 8: 9b_Pl: *
 9: 9b_pr: *
 10: 9b_ro: *
 11: 9b_sts: *
 12: 9b_sy: *
 13: 9b_in: *
 14: 9b_vl: *
 15: em_ba: *
 16: em_futn: *
 17: em_hum: *
 18: em_in: *
 19: em_mu: *
 20: em_om: *
 21: em_or: *
 22: em_ov: *
 23: em_pat: *
 24: em_ph: *
 25: em_Dl: *
 26: em_ro: *
 27: em_sts: *
 28: em_un: *
 29: em_vl: *

		% Result No.			Score Match Length DB ID			Description	
								SUMMARIES	
		1	2065	100.0	2065	6	AX454630	Sequence	AX491108 Sequence
		2	2065	100.0	2065	6	AX491108	Sequence	AX697151 Sequence
		3	2065	100.0	2065	6	AX697151	Sequence	AY355227 Homo sapi
		4	1318.4	63.8	117854	9	AY358527	Homo sapi	AL117383 Human DNA
		5	1318.4	63.8	117854	9	RSUJB85A10		BC047076 Homo sapi
		6	873	42.3	926	9	BC047076	Homo sapi	AC015860 Homo sapi
		7	758.8	36.7	248469	2	AC015860	Homo sapi	AL929097 Mouse DNA
		8	615.6	29.8	183553	2	AC012335	Homo sapi	AC117551 Mus muscu
		9	614	29.7	614	6	AX317844	Sequence	AC106497 Continuation (3 of
		10	614	29.7	614	6	AX419522	Sequence	AC135745 Rattus no
		11	609.4	29.5	611	6	AX498264	Sequence	AX402346 Sequence
		12	608	29.4	107504	10	AY134633	Mus muscu	AY134633 Mus muscu
		13	608	29.4	222104	10	AL929154		AC012335 Homo sapi
		14	608	29.4	256869	2	AC117551		AC117551 Mus muscu
		15	594.6	28.8	110000	2	AC112018		AC106497 Continuation (3 of
		16	571.4	27.7	222922	2	AC106497	Rattus no	AC135745 Rattus no
		17	571.4	27.7	245485	2	AC135745		AX047076 Sequence
		18	520.8	25.2	1286	6	AY134633		AY134633 Mus muscu
		19	514.2	24.9	808	10	AY134663		AC012335 Homo sapi
		20	492.2	23.8	183553	2	AC012335		AR414692 Sequence
		21	477.8	23.1	493	6	BD110245	EST and e	BD110245 EST and e
		22	477.8	23.1	493	6	AC015860	Homo sapi	AC015860 Homo sapi
		23	455.4	22.1	248469	2	BC056851	Xenopus laevis	BC056851 Xenopus laevis
		24	375.2	18.2	1805	10	BC055682	Mus muscu	BC055682 Mus muscu
		25	292.4	14.2	1810	10	BC035789	Homo sapi	BC035789 Homo sapi
		26	291.2	14.1	2423	9	AX018985	Sequence	AX018985 Sequence
		27	289.8	14.0	2484	6	BD135080	Cerebellum	BD135080 Cerebellum
		28	289.8	14.0	2484	6	AK125422	Homo sapi	AK125422 Homo sapi
		29	289.8	14.0	2750	6	AX463952	Sequence	AX463952 Sequence
		30	289.8	14.0	2750	9	AY359074	Homo sapi	AY359074 Homo sapi
		31	257.4	12.5	1524	9	M58581	Human prece	M58581 Human prece
		32	254.8	12.3	2056	10	BC055730	Mus muscu	BC055730 Mus muscu
		33	253.6	12.3	1266	5	BC054117	Xenopus laevis	BC054117 Xenopus laevis
		34	239.2	11.6	2430	10	BC051956	Mus muscu	BC051956 Mus muscu
		35	154.4	7.5	3336	9	AK125422	Homo sapi	AK125422 Homo sapi
		36	152.6	7.4	285	6	AX913514	Sequence	AX913514 Sequence
		37	152.6	7.4	285	6	BD049127	Sequence	BD049127 Sequence
		38	151.6	7.3	265	10	S76975	Mus sp: cerebellum	S76975 Mus sp: cerebellum
		39	145.6	7.1	16732	5	AL929379	Zebrafish	AL929379 Zebrafish
		40	145.2	7.0	181602	9	AC011208	Homo sapi	AC011208 Homo sapi
		41	134.2	6.5	234942	10	AC115783		AC115783
		42	132.8	6.4	165651	9	AC044798	Homo sapi	AC044798 Homo sapi
		43	132.8	6.4	185418	2	AC012311	Homo sapi	AC012311 Homo sapi
		44	132.8	6.4	192347	9	AC007614	Homo sapi	AC007614 Homo sapi
		45	130	6.3	1384	6	BD193129	human	BD193129 human

ALIGNMENTS

RESULT 1	AX454630	DEFINITION	2065 bp	DNA	linear	PAT 06-JUL-2002
LOCUS	AX454630	SEQUENCE	215 from Patent WO0203284.			
ACCESSION	AX454630	VERSION	GI:21713339			
KEYWORDS		SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1	AUTHORS	Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillian,K.J., Marsers,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.			

Pred. No. is the number of results predicted by chance to have a

QY	1861	TTTAAAGGGCTCTGGTGTATTGAGGTATCCTGGTTGCCCTAACCTTTAAATTG	1981
Db	1861	TTTCAAGGCTTCGTGTATTGAGGTATCCTGGTTGCCCTAACCTTTAAATTG	1924
QY	1921	TATATATTATCTCTGTTAGCTAATTAATTCAATAATTCCATATCTTAATTCTAGCCA	1981
Db	1921	TATATATTATCTCTGTTAGCTAATTAATTCAATAATTCCATATCTTAATTCTAGCCA	1981
QY	1981	ATATCTTGCTCTTGTATAGCTCATATGAATTCTATAATTATTATGCTGTATAGAA	204
Db	1981	ATATCTTGCTCTTGTATAGCTCATATGAATTCTATAATTATTATGCTGTATAGAA	204
QY	2041	TAAGATTATATATGGTTAAAAAA	2065
Db	2041	TAAGATTATATATGGTTAAAAAA	2065
RESULT 2			
	AX491108	AX491108	AX491108
LOCUS	AX491108	2065 bp	DNA
DEFINITION	Sequence 215 from Patent WO200690.	linear	PAT 16-AUG-2000
ACCESSION	AX491108		
VERSION	AX491108.1	GI:22323891	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiridae; Homo.		
REFERENCE	Baker,K.P., Ferrara,N., Gerber,R., Gerritsen,M.E., Goddard,A., Godowski,P.J.J., Gurney,A.L., Hillian,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I., and Ye,W.		
AUTHORS			
TITLE	Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis		
JOURNAL	Patent: WO 200690-A 215 03-JUN 2002;		
FEATURES	Genentech, Inc. (US)		
source	Location/Qualifiers		
	1. 2065		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
Query Match			
Best Local Similarity	100.0%	Score 2065;	DB 6;
Matches	100.0%	Pred. No. 0;	Length 2065;
	Conservative	Mismatches 0;	Indels 0;
		Gaps 0;	
QY	1	GTGAATCTGAGGGTTATGACTTTCAGATGTTAGGACCAAGTGTGGCTGTGAGGGCC	60
Db	1	GTGAATCTGAGGGTTATGACTTTCAGATGTTAGGACCAAGTGTGGCTGTGAGGGCC	60
QY	61	CAGGCAGGCTATTCTGGCGGAGGAGTAGGTAAAGGGTTCTGATGAGCTCTT	120
Db	61	CAGGCAGGCTATTCTGGCGGAGGAGTAGGTAAAGGGTTCTGATGAGCTCTT	120
QY	121	AAAGGACAAGGTAACAGGCGGAGGAGCTCGAGGGAGACTTGAAGCTCAAGCCA	180
Db	121	AAAGGACAAGGTAACAGGCGGAGGAGCTCGAGGGAGACTTGAAGCTCAAGCCA	180
QY	181	CAGAAATTGGTGAAGGTGCGGCCGCGCCGCTCTCTGAGGGCTGTGACCTA	240
Db	181	CAGAAATTGGTGAAGGTGCGGCCGCGCCGCTCTCTGAGGGCTGTGACCTA	240
QY	241	GCGCTAGCATCTCCGAGAACGGATCCGGGTAGGAGGCCATGGCGGAGCAC	300
Db	241	GCGCTAGCATCTCCGAGAACGGATCCGGGTAGGAGGCCATGGCGGAGCAC	300
QY	301	AGGCCAGCGGCTGGCTGCCAACAGGGCTCACATGGCTGCCAGGGCTG	360
Db	301	AGGCCAGCGGCTGGCTGCCAACAGGGCTCACATGGCTGCCAGGGCTG	360
QY	361	TCCGCGGTGCGGCCGCTCAAGGCGGGCTCTCAAGGCGGGCTGCGGCCAG	420

QY	1081	GCTGGAACCAATACAATTACAGATTATTGTGTCAGTATTGGAA	1140	ACCESSION	AY358527
Db	1081	GCTGGAACCAATACAATTACAGATTATTGTGTCAGTATTGGAA	1140	VERSION	AY358527..1
QY	1141	TGGGACTCTAACGAGATAATACCTATGCTTAAGTCAAGTGTGAA	1200	KEYWORDS	GI:37182176
Db	1141	TGGGACTCTAACGAGATAATACCTATGCTTAAGTCAAGTGTGAA	1200	SOURCE	Eukaryota; Chordata; Craniata; Vertebrata; Butteleostomi;
QY	1201	ACTTATTCTGATTTCTGGATTACTGAAATTGATAGTGTGGAAATT	1260	ORGANISM	Homo sapiens (human)
Db	1201	ACTTATTCTGATTTCTGGATTACTGAAATTGATAGTGTGGAAATT	1260	REFERENCE	Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currel, B., Deue, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P.E., Heldens, S., Huang, A., Kim, H.S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Marx, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandalen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Godowski, A., Wood, W.I. and Godowski, P.
QY	1261	TGTTAGTTAACAGCTGGCAACCGGTTAACGTTAACCTAAAGTCTGAC	1320	AUTHORS	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
Db	1261	TGTTAGTTAACAGCTGGCAACCGGTTAACGTTAACCTAAAGTCTGAC	1320	JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)
QY	1321	TTCATCAACCGTTAGTGATACTGCAAGAAGTCTGTTATATGATT	1380	PUBLISHED	12975309
Db	1321	TTCATCAACCGTTAGTGATACTGCAAGAAGTCTGTTATATGATT	1380	REFERENCES	2 (bases 1 to 2065)
QY	1381	ATATTCGTTTATCCCTTGGAAATTAGTGTGAAACTGGATT	1440	AUTHORS	Clark, H.F.
Db	1381	ATATTCGTTTATCCCTTGGAAATTAGTGTGAAACTGGATT	1440	TITLE	Direct Submission
QY	1441	TTTTTCAGAACCTGTTCTCTAAATAAGTGTAACTGCTCCAC	1500	JOURNAL	Submitted (01-Aug-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Db	1441	TTTTTCAGAACCTGTTCTCTAAATAAGTGTAACTGCTCCAC	1500	FEATURES	Location/Qualifiers
QY	1501	AAATTTACCTTGACTAGATACTGACATGCACTCTCCTCAA	1560	source	1. 2065
Db	1501	AAATTTACCTTGACTAGATACTGACATGCACTCTCCTCAA	1560	organism	"Homo sapiens"
QY	1561	TAGTGTATTAACTGTTATGCTTAAAGTGTATTTCTAAAA	1620	mol_type	"tRNA"
Db	1561	TAGTGTATTAACTGTTATGCTTAAAGTGTATTTCTAAAA	1620	db_xref	"taxon:2606"
QY	1621	AGAAAGAATAGCATATAATTGTGACAGGAAAAGTTGCTTACCGAA	1680	/clone	"IDNA6526"
Db	1621	AGAAAGAATAGCATATAATTGTGACAGGAAAAGTTGCTTACCGAA	1680	gene	1..2055
QY	1681	ATCCCTGACCTTACGAAAGTCTGTTATTTCTCAAGTAA	1740	CDS	/locus_tag="UNQ718"
Db	1681	ATCCCTGACCTTACGAAAGTCTGTTATTTCTCAAGTAA	1740	product	"GSGR718"
QY	1741	CTTTAAATTAAAATGTTGAAATTAAACCACTTTAAACCTTAAGTGT	1800	protein_id	"AAQ8891_1"
Db	1741	CTTTAAATTAAAATGTTGAAATTAAACCACTTTAAACCTTAAGTGT	1800	db_xref	"GI:37182177"
QY	1801	CGTAGACATGACCCTTAACTGGTGTGGATGCTTACCAT	1860	translation	"MSGRRALSAVPAVLLVLITLPGIPWQAONDTEBIVLEGKCLVYCDSNPATOSKGSSSPPLISVRAANSKVAQTSVNLNEKPVIAFGRKDVTREAATNGVLLYLQEDKVYLKLEKGNLNVGGWQYSTFSGEFLVFPL"
Db	1801	CGTAGACATGACCCTTAACTGGTGTGGATGCTTACCAT	1860	ORIGIN	
QY	1861	TTTCGAAGGTTCTGTTGATTTGAGTATCATCGCTTAACCTTAAATTG	1920	Query Match	100..0%
Db	1861	TTTCGAAGGTTCTGTTGATTTGAGTATCATCGCTTAACCTTAAATTG	1920	Best Local Similarity	100..0%
QY	1921	TATATTTATCTGTTAGCTTAAATTCAATCCATATCTAAATTG	1980	Matches	205;
Db	1921	TATATTTATCTGTTAGCTTAAATTCAATCCATATCTAAATTG	1980	Conservative	0;
QY	1981	ATATCTGTTGCTTGTAGCTTAAATTCAATCCATATCTAAATTG	2040	Mismatches	0;
Db	1981	ATATCTGTTGCTTGTAGCTTAAATTCAATCCATATCTAAATTG	2040	Indels	0;
QY	2041	TAAGTATAATATGTAAAAAA	2065	Gaps	0;
Db	2041	TAAGTATAATATGTAAAAAA	2065		
RESULT 4					
AY358527					
LOCUS					
DEFINITION					

7
page

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

EMLI; Swi: SWISSPROT; Tr: TREMBL; Wp: WORMPBP; Information on the WORMPBP database can be found at <http://www.sanger.ac.uk/Projects/C/elegans/wormped>. This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chromosome_20.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred Quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP5-885A10 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2

IMPORTANT: This sequence is not the entire insert of clone RP5-885A10. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP5-885A10 is at 1 in this sequence. The true left end of clone RP11-380D15 is at 117755 in this sequence. The true right end of clone RP11-458E15 is at 27524 in this sequence.

misc_feature	/note="match: GSS: Em: B58489"	Db	1526 GGAACCAAGGTCTAAGGATTAGAAAACCTCAATGAACTTCATGTTAGTGT 1467
misc_feature	/note="match: GSS: Em: AQ8993089"	Qy	1340 GAACTGCAGAACGACTATACTGTGTTATATGGATTATACTTGTTATTCCCT 1399
repeat_region	24942..252279	Db	1466 GAACTGCAGAACGACTATACTGTGTTATATGGATTATACTTGTTATTCCCT 1407
repeat_region	2588..6161	Qy	1400 TGAATTAGTTGTTGGTTCTGTAAAAAACTGGATTTTTCACTGGTAT 1459
repeat_region	26231..26402	Db	1406 TGAAATTAGTTGTTGGTTCTGTAAAAAACTGGATTTTTCACTGGTAT 1347
repeat_region	/MER3 repeat: matches 5..176 of consensus"	Db	
repeat_region	/note="T12 repeat: matches 5388..6155 of consensus"	Qy	1460 TAGTTTCTPAAATAAGGTAATGATGGCTGCCAACAAATTACCTGACTAGCA 1519
repeat_region	complement(27157..27515)	Db	1346 TAGTTTCTPAAATAAGGTAATGATGGCTGCCAACAAATTACCTGACTAGCA 1287
repeat_region	/note="AluSx repeat: matches 1..285 of consensus"	Db	1520 TACATGGACATGACITCTCAAAAAAAAAAGTTGCTCATGTTCTATTATGCTA 1579
repeat_region	27585..27738	Qy	
repeat_region	/note="Aluy repeat: matches 147..300 of consensus"	Db	1286 TACATGACATGACITCTCAAAAAAAAAAGTTGCTCATGTTCTATTATGCTA 1227
repeat_region	27744..27934	Qy	
repeat_region	/note="LJ repeat: matches 2555..2750 of consensus"	Db	1580 TAGTGAAAGAGTCATAATTTCOAGTTATTTCTAAGAGAGATACTCATATAAT 1639
repeat_region	28859..29039	Qy	
misc_feature	/note="MIR repeat: matches 1..218 of consensus"	Db	1226 TAGTGAAAGAGTCATAATTTCOAGTTATTTCTAAGAGAGATACTCATATAAT 1167
repeat_region	complement(29154..29702)	Db	
repeat_region	/note="match: GSS: Em: AQ853339"	Qy	1640 CTCACAGGAAAMAAGTGTCTACCCAAATCTAAGTCTCAATCCCTGAGCCTAGCAA 1699
repeat_region	29329..29553	Db	1166 CTGACAGGAAAMAAGTGTCTACCCAAATCTAAGTCTCAATCCCTGAGCCTAGCAA 1107
misc_feature	/note="MIR repeat: matches 32..262 of consensus"	Db	
repeat_region	29593..30173	Qy	
repeat_region	/note="match: GSS: Em: AQ052168"	Db	1700 ACAGCTCCCTCCGAGGAAATCTTACACTTTAGTGTCACTTTAATTAAATGATTGA 1759
repeat_region	match: SRS: Em: AQ052168	Db	1106 ACAGCTCCCTCCGAGGAAATCTTACACTTTAGTGTCACTTTAATTAAATGATTGA 1047
repeat_region	29658..29737	Qy	
repeat_region	/note="MER96 repeat: matches 1..71 of consensus"	Db	
Query_Match	63..91%; Score 1318..4; DB 9; Length 117854;	Qy	1760 TAATAACCACITTAATAAAACCTAAAGGTTTTTCCGTTGACATGACACCTTA 1819
Best_Local_Similarity	99..98%; Pred. No.: 2e-222;	Db	1046 TAATAACCACITTAATAAAACCTAAAGGTTTTTCCGTTGACATGACACCTTA 987
Matches_1319:	Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy	
Db		1820 TTAACCTGGTGGATGGCTGCTTTCTTCAATTATACCTTAAAGGTTTTGCTGTGT 1879	
Qy	740 TCGAGGTTAACITGATGTTAAATGGAAACCACTAAATCTGCTCTGGGGGACAAG 799	Db	986 TTAACCTGGTGGATGGCTGCTTTCTTCAATTATACCTTAAAGGTTTTGCTGTGT 927
Db	2066 TTAGGTAAACTGTGATGTTAAATGGAAACCACTAAATCTGCTCTGGGGGACAAG 2007	Qy	
Qy	800 ATGTTACCTCGTAGAGCTGCCACAAATGTTCTGCTCTACCTGAAAGGATAAG 859	Db	1880 ATTGGAGTATCATCGGTGTTGCCCTAACCTTAATTGTTATTTATCTGTTAG 1939
Db	2006 ATGTTACCTCGTAGAGCTGCCACAAATGTTCTGCTCTACCTGAAAGGATAAG 859	Db	926 ATTGGAGTATCATCGGTGTTGCCCTAACCTTAATTGTTATTTATCTGTTAG 867
Qy	860 TTATACCTAAACTGGAAAGGTAATTTGGTGGAGCTGGAGTATCCAGTTCTG 919	Qy	1940 CTAAATTAATTCAATAATCCCATCTAAATGTTGCTGAAATCTGGTTTGTATA 1999
Db	1946 TTATACCTAAACTGGAAAGGTAATTTGGTGGAGCTGGAGTATCCAGTTCTG 919	Db	866 CTAAATTAATTCAATAATCCCATCTAAATGTTGCTGAAATCTGGTTTGTATA 807
Qy	920 GTTTTCGGTGTCCCCCTATGGATTAAATCTCCATGATGTTCCAGGTGAGGA 979	Qy	2000 GGTATGAAATTCAAATAATTATTTATGTCGTTAGATAAGATAATAATATGTTA 2059
Db	1886 GCTTTCTGGTGTCCCCCTATGGATTAAATCTCCATGATGTTCCAGGTGAGGA 1827	Db	806 GTCATGAAATTCAAATAATTATGTCGTTAGATAAGATAATAATATGTTA 747
Qy	980 TGACCCACTCTGAGTATTGGAAAGATCATTTTCATCATTGGATTGATCTTTATT 1039	RESULT 6	
Db	1826 TGACCCACTCTGAGTATTGGAAAGATCATTTTCATCATTGGATTGATCTTTATT 1767	BC047076 LOCUS	BC047076 mRNA
Qy	1040 GTTTCTCATGGTGTGGATATGGATTCTAGGTTCTGCTAACCAATACAAAT 1099	JOURNAL	Homo sapiens, cDNA IMAGE: 5314390, mRNA.
Db	1766 GTTTCTCATGGTGTGGATATGGATTCTAGGTTCTGCTAACCAATACAAAT 1707	DEFINITION	Gene Collection (M3C)
Qy	1100 TTACAGATTATTGGTGTGGCTCAAAAGCTGTCAGTAAATTCAGGAGATA 1159	ACCESSION	BC047076
Db	1706 TTACAGATTATTGGTGTGGCTCAAAAGCTGTCAGTAAATTCAGGAGATA 1647	VERSION	BC047076..1 GI:28436739
Qy	1160 ATACCTGCTAAATGTAAGTCAAAAGCTGTCAGTAAATTCAGGAGATA 1219	KEYWORDS	
Db	1646 ATACCTGCTAAATGTAAGTCAAAAGCTGTCAGTAAATTCAGGAGATA 1587	ORGANISM	Homo sapiens (human)
Qy	1220 TCCTGGGATTACTGATGTTACGATGTTGCTGCTGTTAAAGACT 1279	AUTHORS	Strausberg, R.
Db	1586 TCCTGGGATTACTGATGTTACGATGTTGCTGCTGTTAAAGACT 1527	TITLE	Direct Submission
Qy	1280 GGCAACCAGGCTTAAGGATTAGAAAACCTCAATCAAGGTAGTGT 1339	JOURNAL	Submitted (19-FEB-2003) National Institutes of Health, Mammalian Gene Collection (M3C), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
Db		COMMENT	NIH-M3C Project URL: http://mgc.nci.nih.gov
Qy		REMARK	Contact: MGCG help desk
		COMMENT	Email: cgabbs@mail.nih.gov
		REMARK	Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)	Db	600	CTTATTAACCTTAAGG-TTTTTTTCGGTACATGCCATTATAAATGGT	
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNN)	Qy	1829	GTTGGATGCGTTCTGTCTATTACCTTCAAGGCTCTGTGATTGAACTT	
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center	Db	659	GTTGGATGCGTTCTGTCTATTACCTTCAAGGCTCTGTGATTGAACTT	
Center code: BCM-HGSC	Qy	1889	ATCATCGGTTAACCTTAATGTTAGCTTAATGTTAGCTATGATTA	
Web site: http://www.hgsc.bcm.edu/cdna/	Db	719	ATCATCGGTTAACCTTAATGTTAGCTTAATGTTAGCTATGATTA	
Contact: amg@bcm.tmc.edu	Qy	1949	AATTCAAATCCATTAATGTTAGCTTAATGTTAGCTATGATTA	
Ganarathne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowals, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.	Db	779	AATTCAAATCCATTAATGTTAGCTTAATGTTAGCTATGATTA	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNN at: http://image.llnl.gov	Qy	2009	AATTCAAATCCATTAATGTTAGCTTAATGTTAGCTATGATTA	
Series: IRAK Plate: 91 Row: o Column: 23.	Db	839	AATTCAAATCCATTAATGTTAGCTTAATGTTAGCTATGATTA	
Location/Qualifiers			895	
1.. 926				
/organism="Homo sapiens"				
/mol type="mRNA"				
/db xref="taxon:9606"				
/clone "IMAGE:5314390"				
/tissue type="Brain, hypothalamus"				
/clone lib="NIH MGC_96"				
/lab_hst= DH10B				
/note="Vector: pBluescript"				
FEATURES				
source				
ORIGIN				
Query Match Score 873; DB 9; Length 926;				
Best Local Similarity 99.8%;				
Matches 895; Conservative 0; Mismatches 0;				
Indels 2; Gaps 2;				
DBY				
1169 CTTAAATGAACTGCAAAAGCTGTCGGAAACTTCTGAATTCAATTCGGAT 1228				
1 CTTAAATGAACTGCAAAAGCTGTCGGAAACTTCTGAATTCAATTCGGAT 60				
DBZ				
1229 TACTGAACTGAGCTGAGATTTAGTTAACACTGCCAACCG 1288				
61 TACTGAACTGAGCTGAGATTTAGTTAACACTGCCAACCG 120				
DBY				
1289 GTCTAAAGGTTGAAACTCTAAAGTCTGACTTCATAACCGTTAGTGATACTGC 1348				
121 GTCTAAAGGTTGAAACTCTAAAGTCTGACTTCATAACCGTTAGTGATACTGC 180				
DBZ				
1349 AAAGAACTCTATACTGTGTTTATATGTTATTATGTTTGTGAAATTAG 1408				
181 AAAGAACTCTATACTGTGTTTATATGTTATTATGTTTGTGAAATTAG 239				
DBY				
1409 TTGTGTTGTTCTGTAAACACTGGATTTTCTGACTGTTATGTTCTGACTGC 1468				
240 TTGTGTTGTTCTGTAAACACTGGATTTTCTGACTGTTATGTTCTGACTGC 299				
DBZ				
1469 TCTTAAATAAACTGAAATGTTACCTGACTGATTCATCGA 1528				
300 TCTTAAATAAACTGAAATGTTACCTGACTGATTCATCGA 359				
DBY				
1529 CATGACTCTCTCAAAAAAAAGATGCTCATGTTGATTAACTGTTAGCTGAA 1588				
360 CATGACTCTCTCAAAAAAAAGATGCTCATGTTGATTAACTGTTAGCTGAA 419				
DBZ				
1589 GAGCTATTTCCAAGTAACTTCAAAATCTAAGTCTGAACTGACAGG 1648				
420 GAGCTATTTCCAAGTAACTTCAAAATCTAAGTCTGAACTGACAGG 479				
DBY				
1649 AAAAGTGTCTTCAAAATCTAAGTCTGAACTTCAAAACAGCTCCC 1708				
480 AAAAGTGTCTTCAAAATCTAAGTCTGAACTTCAAAACAGCTCCC 539				
DBZ				
1709 CTCCGAGGAAATCTTACTCTTATGCTCAACTTAACTGATGATAACCA 1768				
540 CTCCGAGGAAATCTTACTCTTATGCTCAACTTAACTGATGATAACCA 539				
DBY				
1769 CTTTAAANACCTTAAAGCTTAACTGTTAGCTTAACTGTTAGCTTAACTGTT 1828				
DBZ				

* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

**	861:	contig of 863 bp in length	35252:	contig of 893 bp in length
**	963:	gap of 100 bp	35253:	gap of 100 bp
**	1841:	contig of 878 bp in length	35254:	contig of 862 bp in length
**	1942:	gap of 100 bp	36215:	gap of 100 bp
**	2831:	contig of 890 bp in length	36314:	gap of 100 bp
**	2932:	gap of 100 bp	37222:	contig of 908 bp in length
**	3755:	contig of 824 bp in length	37223:	gap of 100 bp
**	3856:	gap of 100 bp	38320:	contig of 998 bp in length
**	4751:	contig of 895 bp in length	38321:	gap of 100 bp
**	5744:	contig of 894 bp in length	39106:	contig of 986 bp in length
**	5745:	gap of 100 bp	39107:	gap of 100 bp
**	6713:	contig of 869 bp in length	39407:	contig of 870 bp in length
**	6813:	gap of 100 bp	40276:	contig of 870 bp in length
**	7714:	contig of 902 bp in length	40376:	gap of 100 bp
**	7815:	gap of 100 bp	40377:	contig of 895 bp in length
**	8092:	contig of 877 bp in length	41371:	gap of 100 bp
**	8693:	gap of 100 bp	41372:	contig of 884 bp in length
**	9674:	contig of 862 bp in length	42255:	gap of 100 bp
**	9675:	gap of 100 bp	42256:	contig of 870 bp in length
**	10655:	contig of 882 bp in length	43225:	gap of 100 bp
**	10757:	gap of 100 bp	43226:	contig of 861 bp in length
**	11630:	contig of 874 bp in length	44196:	contig of 895 bp in length
**	11631:	gap of 100 bp	44187:	gap of 100 bp
**	12610:	contig of 880 bp in length	44287:	contig of 896 bp in length
**	12710:	gap of 100 bp	45183:	gap of 100 bp
**	13622:	contig of 912 bp in length	45283:	contig of 909 bp in length
**	13723:	gap of 100 bp	46191:	contig of 909 bp in length
**	14593:	contig of 870 bp in length	46192:	gap of 100 bp
**	14663:	gap of 100 bp	46291:	contig of 900 bp in length
**	15567:	contig of 875 bp in length	47271:	contig of 860 bp in length
**	15568:	gap of 100 bp	47272:	contig of 896 bp in length
**	16420:	contig of 753 bp in length	48137:	contig of 896 bp in length
**	16421:	gap of 100 bp	48138:	gap of 100 bp
**	17444:	contig of 924 bp in length	48237:	gap of 100 bp
**	17445:	gap of 100 bp	48238:	contig of 909 bp in length
**	17545:	contig of 878 bp in length	49176:	contig of 909 bp in length
**	18423:	gap of 100 bp	49276:	gap of 100 bp
**	19453:	contig of 941 bp in length	50214:	contig of 936 bp in length
**	19564:	gap of 100 bp	50215:	contig of 901 bp in length
**	20473:	gap of 100 bp	51073:	contig of 759 bp in length
**	20572:	contig of 100 bp	51074:	gap of 100 bp
**	2144:	contig of 872 bp in length	52022:	contig of 849 bp in length
**	2145:	gap of 100 bp	52023:	gap of 100 bp
**	22435:	contig of 890 bp in length	52122:	gap of 100 bp
**	22535:	gap of 100 bp	52123:	contig of 936 bp in length
**	23414:	contig of 909 bp in length	53012:	contig of 890 bp in length
**	23514:	gap of 100 bp	53013:	contig of 100 bp
**	23515:	contig of 842 bp in length	53112:	gap of 100 bp
**	24456:	gap of 100 bp	54014:	contig of 901 bp in length
**	24545:	contig of 873 bp in length	54114:	gap of 100 bp
**	25330:	gap of 100 bp	55000:	contig of 887 bp in length
**	25339:	contig of 890 bp in length	55001:	gap of 100 bp
**	28292:	gap of 100 bp	55072:	contig of 872 bp in length
**	28292:	contig of 886 bp in length	55973:	gap of 100 bp
**	26315:	contig of 100 bp	56072:	contig of 876 bp in length
**	26316:	contig of 907 bp in length	56073:	contig of 901 bp in length
**	27322:	contig of 842 bp in length	57048:	gap of 100 bp
**	27422:	gap of 100 bp	57945:	contig of 897 bp in length
**	28291:	contig of 869 bp in length	58045:	gap of 100 bp
**	28291:	gap of 100 bp	58046:	contig of 884 bp in length
**	29255:	contig of 864 bp in length	58930:	gap of 100 bp
**	29256:	gap of 100 bp	59029:	contig of 100 bp
**	29316:	contig of 842 bp in length	59030:	contig of 898 bp in length
**	30235:	contig of 879 bp in length	59928:	gap of 100 bp
**	30235:	gap of 100 bp	60027:	contig of 895 bp in length
**	31224:	contig of 890 bp in length	60928:	contig of 948 bp in length
**	31225:	gap of 100 bp	61066:	contig of 956 bp in length
**	31324:	contig of 869 bp in length	61076:	gap of 100 bp
**	31325:	contig of 931 bp in length	61166:	gap of 100 bp
**	32255:	contig of 937 bp in length	61147:	contig of 981 bp in length
**	32256:	gap of 100 bp	61918:	contig of 100 bp
**	33282:	contig of 877 bp in length	62018:	gap of 100 bp
**	33283:	gap of 100 bp	62028:	contig of 933 bp in length
**	34229:	contig of 877 bp in length	70218:	gap of 100 bp
**	34233:	gap of 100 bp	70219:	contig of 898 bp in length
**	34260:	gap of 100 bp	71216:	contig of 898 bp in length

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em : EMBL; Sw : SWISSPROT; Tr : TREMBL; Wp : WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep RP23-76M8 is constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

FEATURES
VECTOR: pBACe3.6.
Location/Qualifiers
1. 101500 /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="2"
/clone="RP23-76M8"
/clone_lib="RPCI-23"

source	ORIGIN	Query Match	Score	Length	Pred.	No.	Mismatches	Indels	Gaps	16;	16.2	16.4	16.6	16.8	17.0	17.2	17.4	17.6	17.8	18.0	18.2	18.4	18.6	18.8	19.0	19.2	19.4	19.6	19.8	20.0	20.2	20.4	20.6	20.8	21.0	21.2	21.4	21.6	21.8	22.0	22.2	22.4	22.6	22.8	23.0	23.2	23.4	23.6	23.8	24.0	24.2	24.4	24.6	24.8	25.0	25.2	25.4	25.6	25.8	26.0	26.2	26.4	26.6	26.8	27.0	27.2	27.4	27.6	27.8	28.0	28.2	28.4	28.6	28.8	29.0	29.2	29.4	29.6	29.8	29.9	30.0	30.1	30.2	30.3	30.4	30.5	30.6	30.7	30.8	30.9	31.0	31.1	31.2	31.3	31.4	31.5	31.6	31.7	31.8	31.9	32.0	32.1	32.2	32.3	32.4	32.5	32.6	32.7	32.8	32.9	33.0	33.1	33.2	33.3	33.4	33.5	33.6	33.7	33.8	33.9	34.0	34.1	34.2	34.3	34.4	34.5	34.6	34.7	34.8	34.9	35.0	35.1	35.2	35.3	35.4	35.5	35.6	35.7	35.8	35.9	36.0	36.1	36.2	36.3	36.4	36.5	36.6	36.7	36.8	36.9	37.0	37.1	37.2	37.3	37.4	37.5	37.6	37.7	37.8	37.9	38.0	38.1	38.2	38.3	38.4	38.5	38.6	38.7	38.8	38.9	39.0	39.1	39.2	39.3	39.4	39.5	39.6	39.7	39.8	39.9	39.10	39.11	39.12	39.13	39.14	39.15	39.16	39.17	39.18	39.19	39.20	39.21	39.22	39.23	39.24	39.25	39.26	39.27	39.28	39.29	39.30	39.31	39.32	39.33	39.34	39.35	39.36	39.37	39.38	39.39	39.40	39.41	39.42	39.43	39.44	39.45	39.46	39.47	39.48	39.49	39.50	39.51	39.52	39.53	39.54	39.55	39.56	39.57	39.58	39.59	39.60	39.61	39.62	39.63	39.64	39.65	39.66	39.67	39.68	39.69	39.70	39.71	39.72	39.73	39.74	39.75	39.76	39.77	39.78	39.79	39.80	39.81	39.82	39.83	39.84	39.85	39.86	39.87	39.88	39.89	39.90	39.91	39.92	39.93	39.94	39.95	39.96	39.97	39.98	39.99	39.100	39.101	39.102	39.103	39.104	39.105	39.106	39.107	39.108	39.109	39.110	39.111	39.112	39.113	39.114	39.115	39.116	39.117	39.118	39.119	39.120	39.121	39.122	39.123	39.124	39.125	39.126	39.127	39.128	39.129	39.130	39.131	39.132	39.133	39.134	39.135	39.136	39.137	39.138	39.139	39.140	39.141	39.142	39.143	39.144	39.145	39.146	39.147	39.148	39.149	39.150	39.151	39.152	39.153	39.154	39.155	39.156	39.157	39.158	39.159	39.160	39.161	39.162	39.163	39.164	39.165	39.166	39.167	39.168	39.169	39.170	39.171	39.172	39.173	39.174	39.175	39.176	39.177	39.178	39.179	39.180	39.181	39.182	39.183	39.184	39.185	39.186	39.187	39.188	39.189	39.190	39.191	39.192	39.193	39.194	39.195	39.196	39.197	39.198	39.199	39.200	39.201	39.202	39.203	39.204	39.205	39.206	39.207	39.208	39.209	39.210	39.211	39.212	39.213	39.214	39.215	39.216	39.217	39.218	39.219	39.220	39.221	39.222	39.223	39.224	39.225	39.226	39.227	39.228	39.229	39.230	39.231	39.232	39.233	39.234	39.235	39.236	39.237	39.238	39.239	39.240	39.241	39.242	39.243	39.244	39.245	39.246	39.247	39.248	39.249	39.250	39.251	39.252	39.253	39.254	39.255	39.256	39.257	39.258	39.259	39.260	39.261	39.262	39.263	39.264	39.265	39.266	39.267	39.268	39.269	39.270	39.271	39.272	39.273	39.274	39.275	39.276	39.277	39.278	39.279	39.280	39.281	39.282	39.283	39.284	39.285	39.286	39.287	39.288	39.289	39.290	39.291	39.292	39.293	39.294	39.295	39.296	39.297	39.298	39.299	39.300	39.301	39.302	39.303	39.304	39.305	39.306	39.307	39.308	39.309	39.310	39.311	39.312	39.313	39.314	39.315	39.316	39.317	39.318	39.319	39.320	39.321	39.322	39.323	39.324	39.325	39.326	39.327	39.328	39.329	39.330	39.331	39.332	39.333	39.334	39.335	39.336	39.337	39.338	39.339	39.340	39.341	39.342	39.343	39.344	39.345	39.346	39.347	39.348	39.349	39.350	39.351	39.352	39.353	39.354	39.355	39.356	39.357	39.358	39.359	39.360	39.361	39.362	39.363	39.364	39.365	39.366	39.367	39.368	39.369	39.370	39.371	39.372	39.373	39.374	39.375	39.376	39.377	39.378	39.379	39.380	39.381	39.382	39.383	39.384	39.385	39.386	39.387	39.388	39.389	39.390	39.391	39.392	39.393	39.394	39.395	39.396	39.397	39.398	39.399	39.400	39.401	39.402	39.403	39.404	39.405	39.406	39.407	39.408	39.409	39.410	39.411	39.412	39.413	39.414	39.415	39.416	39.417	39.418	39.419	39.420	39.421	39.422	39.423	39.424	39.425	39.426	39.427	39.428	39.429	39.430	39.431	39.432	39.433	39.434	39.435	39.436	39.437	39.438	39.439	39.440	39.441	39.442	39.443	39.444	39.445	39.446	39.447	39.448	39.449	39.450	39.451	39.452	39.453	39.454	39.455	39.456	39.457	39.458	39.459	39.460	39.461	39.462	39.463	39.464	39.465	39.466	39.467	39.468	39.469	39.470	39.471	39.472	39.473	39.474	39.475	39.476	39.477	39.478	39.479	39.480	39.481	39.482	39.483	39.484	39.485	39.486	39.487	39.488	39.489	39.490	39.491	39.492	39.493	39.494	39.495	39.496	39.497	39.498	39.499	39.500	39.501	39.502	39.503	39.504	39.505	39.506	39.507	39.508	39.509	39.510	39.511	39.512	39.513	39.514	39.515	39.516	39.517	39.518	39.519	39.520	39.521	39.522	39.523	39.524	39.525	39.526	39.527	39.528	39.529	39.530	39.531	39.532	39.533	39.534	39.535	39.536	39.537	39.538	39.539	39.540	39.541	39.542	39.543	39.544	39.545	39.546	39.547	39.548	39.549	39.550	39.551	39.552	39.553	39.554	39.555	39.556	39.557	39.558	39.559	39.560	39.561	39.562	39.563	39.564	39.565	39.566	39.567	39.568	39.569	39.570	39.571	39.572	39.573	39.574	39.575	39.576	39.577	39.578	39.579	39.580	39.581	39.582	39.583	39.584	39.585	39.586	39.587	39.588	39.589	39.590	39.591	39.592	39.593	39.594	39.595	39.596	39.597	39.598	39.599	39.600	39.601	39.602	39.603	39.604	39.605	39.606	39.607	39.608	39.609	39.610	39.611	39.612	39.613	39.614	39.615	39.616	39.617	39.618	39.619	39.620	39.621	39.622	39.623	39.624	39.625	39.626	39.627	39.628	39.629	39.630	39.631	39.632	39.633	39.634	39.635	39.636	39.637	39.638	39.639	39.640	39.641	39.642	39.643	39.644	39.645	39.646	39.647	39.648	39.649	39.650	39.651	39.652	39.653	39.654	39.655	39.656	39.657	39.658	39.659	39.660	39.661	39.662	39.663	39.664	39.665	39.666	39.667	39.668	39.669	39.670	39.671	39.672	39.673	39.674	39.675	39.676	39.677	39.678	39.679	39.680	39.681	39.682	39.683	39.684	39.685	39.686	39.687	39.688	39.689	39.690	39.691	39.692	39.693	39.694	39.695	39.696	39.697	39.698	39.699	39.700	39.701	39.702	39.703	39.704	39.705	39.706	39.707	39.708	39.709	39.710	39.711	39.712	39.713	39.714	39.715	39.716	39.717	39.718	39.719	39.720	39.721	39.722	39.723	39.724	39.725	39.726	39.727	39.728	39.729	39.730	39.731	39.732	39.733	39.734	39.735	39.736	39.737	39.738	39.739	39.740	39.741	39.742	39.743	39.744	39.745	39.746	39.747	39.748	39.749	39.750	39.751	39.752	39.753	39.754	39.755	39.756	39.757	39.758	39.759	39.760	39.761	39.762	39.763	39.764	39.765	39.766	39.767	39.768	39.769	39.770	39.771	39.772	39.773	39.774	39.775	39.776	39.777	39.778	39.779	39.780	39.781	39.782	39.783	39.784	39.785	39.786	39.787	39.788	39.789	39.790	39.791	39.792	39.793	39.794	39.795	39.796	39.797	39.798	39.799	39.800	39.801	39.802	39.803	39.804	39.805	39.806	39.807	39.808	39.809	39.810	39.811	39.812	39.813	39.814	39.815	39.816	39.817	39.818	39.819	39.820	39.821	39.822	39.823	39.824	39.825	39.826	39.827	39.828	39.829	39.830	39.831	39.832	39.833	39.834	39.835	39.836	39.837	39.838	39.839	39.840	39.841	39.842	39.843	39.844	39.845	39.846	39.847	39.84

JOURNAL	Submitted (12-SEP-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk
COMMENT	On Sep 16, 2003 this sequence version replaced gi 33412198. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun has only been used where it has a phred quality of at least 30.
Center:	Welcome Trust Sanger Institute
Center code:	SC
Web site:	http://www.sanger.ac.uk
Contact:	humquery@sanger.ac.uk
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.	
This sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.	
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPP; Information on the WORMPP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpp . RP23-4561 is from the RPCL-23 Mouse BAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm .	
VECTOR:	pBAC3.6
FEATURES	
source	1..222104
	/organism="Mus musculus"
	/mol_type="genomic DNA"
	/db_xref="taxon:10090"
	/chromosome="12"
	/clone_id="RP23-4561"
	/clone_lib="RPCI-23"
ORIGIN	
Query Match	29.4%; Score 608; DB 10; Length 222104;
Best Local Similarity	73.6%; Pred. No. 6..9e-97;
Matches 1009; Conservative	0; Mismatches 300; Indels 61; Gaps 16;
QY	737 CTATCGGTTAACTGAGAAGGTAACTGGATTAAATGGAAAACCGTAATATCGCCATTGCGGGGACA 796
DB	113918 CTTTCAGGTTAACTGAAGTAAATGGAAAACCGTAATCTCGATTGGGTATA 113859
QY	797 AAGATGTTACTCCTGTTAAAGCTGCCAACGATGGTGTCTGCTCACTGATAAACAGGATA 856
DB	113858 AAGATGTAACCGTGAAGCGGCCAACGATGGTGTCTGCTCACTGATAAACAGGATA 113799
QY	857 AGGTTTACCTTAAACTGAGAAGGTAACTGGATTAAATGGAAAACCGTAATCTGGATTCCAGGTATT 916
DB	113798 AGGTCTAACCTGAGAAGGTAACTGAGAAGGTAACTGGATTCCAGGTATT 113739
QY	917 CTGGCTTCTGGTGTCTCCCTATAGGATTAATTCTCATGGTGTCTGGATTCCAGGTATT 976
DB	113738 CTGGCTTCTGGTGTCTCCCTATAGAACCAGACTTCGGTGTCTGGATTCCAGGTATT 113679
QY	977 GGATGACGCCACTCCTGAGTATTGGAAAAGATCATTTTCATCATGGTGTCTGGATTCCAGGTATT 1036
DB	113678 CG-----CCACCCCGGGTATAGGATTCAGAAGGACTCTGGATTGATGGTCTGGATTCT 113624
QY	1037 ATGGTTCTCATGGTGTCTGGATTGATTCAGAAGGATTCAGTGGTCTGGACCAATAA 1095

RESULT 14
AC11755/-c

Locus	AC117551	256869 bp DNA linear	HTG 03-MAR-2003
Definition	Mus musculus clone RP23-80N8, WORKING DRAFT SEQUENCE	23 unorderd pieces.	
Accession	AC117551	GT:28631357	
Version	AC117551.5	HTGS PHASPI; HTGS DRAFT.	
Keywords	Mus musculus	(house mouse)	
Source	Mus musculus	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
Organism	Mus musculus	Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.	
Reference	1 (bases 1 to 256869)		
Authors	Birren,B., Birren,B., Nusbaum,C., and Lander,E.		
Title	Mus musculus, clone RP23-80N8		
Journal	Unpublished		
Reference	2 (bases 1 to 256869)		
Authors	Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Chopeel,Y., Colangeli,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeAreilano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Gailagn,J., Garyyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Hulten,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Landers,T., Lehozcy,J., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Margis,N., Matthews,C., McCarthy,M., McEvani,P., McErdle,J., Meldrim,J., Meneus,L., Mihowa,T., Mlense,V., Murphy,T., Naylor,J., Nguyen,C., Nicoll,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.J., Peterson,K., Phankhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Ruse,C., Rosov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schupbach,R., Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N., Straussa,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Vilic,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.		
Title	Direct Submission		
Journal	Submitted [10-APR-2002] Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
Reference	3 (bases 1 to 256869)		
Authors	Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barns,N., Bastien,V., Bloom,T., Boguslavsky,L., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeAreilano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Gaidyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Huime,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Luji,A., Mabbitt,R., Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihowa,T., Mlensa,V., Murphy,T., Naylor,J., Nguyen,C., Nicoll,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phankhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Ruse,C., Rosov,P., Roman,J., Schauer,S., Schupbach,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Strubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.		
Title	Direct Submission		
Journal	Submitted [03-MAR-2003] Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
Comment	All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html		
FEATURES	1. Genome Center Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu	Source	
Location/Qualifiers	1. .organism="Mus musculus" /mol_type="Genomic DNA" /db_xref="Taxon:10090"		

/clone="RP23-80N8"
 /clone.lib="RPCI-23 Female Mouse BAC"
 1. .5629
 /note="assembly_fragment
 clone_end:SP6
 vector_side:left"
 misc_feature
 /note="assembly_fragment"
 5'30. .6454
 misc_feature
 /note="assembly_fragment"
 6555. .7659
 misc_feature
 /note="assembly_fragment"
 7760. .9340
 misc_feature
 /note="assembly_fragment"
 941. .11012
 misc_feature
 /note="assembly_fragment"
 11113. .12227
 misc_feature
 /note="assembly_fragment"
 13028. .14558
 misc_feature
 /note="assembly_fragment"
 14559. .16483
 misc_feature
 /note="assembly_fragment"
 16584. .18111
 misc_feature
 /note="assembly_fragment"
 18212. .20336
 misc_feature
 /note="assembly_fragment"
 20437. .23219
 misc_feature
 /note="assembly_fragment"
 23420. .24224
 misc_feature
 /note="assembly_fragment"
 25025. .28533
 misc_feature
 /note="assembly_fragment"
 28434. .34147
 misc_feature
 /note="assembly_fragment"
 34848. .42292
 misc_feature
 /note="assembly_fragment"
 42393. .54117
 misc_feature
 /note="assembly_fragment"
 55018. .7479
 misc_feature
 /note="assembly_fragment"
 74980. .90551
 misc_feature
 /note="assembly_fragment"
 90552. .108473
 misc_feature
 /note="assembly_fragment"
 108574. .123030
 misc_feature
 /note="assembly_fragment"
 123131. .177280
 misc_feature
 /note="assembly_fragment"
 177381. .225343
 misc_feature
 /note="assembly_fragment"
 215444. .256869
 misc_feature
 /note="assembly_fragment
 clone_end:IV
 vector_side:right"

ORIGIN

Query Match 29.4%; Score 608; DB 2; Length 256869;
 Best Local Similarity 73.6%; Pred. No. 7e-97; Mismatches 0; Indels 61; Gaps 16;

Matches 1009; Conservative 0; Mismatches 300; Indels 61; Gaps 16;

QY 737 CTATCCAGTTAACCTGTGATGTTAAATGGAAAAACCGTAAATCNGCCTTGGGGGAAACA 796
 DB 247240 CTTTCAGGTTAACCTGTGATGTTAAATGGAAAAACCGTAAATCCTGCAATTGGTGTGATA 247181

QY 797 AAGATGTAACTCGGAAGGTGCCAGTACCTGATGTTGGCAAGGATAAAGGATA 856
 DB 247180 AAGATGTGACCCGTTGGATGTTAACCTGTGATGTTGGCAAGGATA 247121

QY 857 AGGTTAACCTAAAATGGAAAGSTAATTGGTGGAGGCTCACGATTCCACGTTT 916
 DB 247120 AGGTACCTAAACTGGAAAGSTAATTGGTGGAGGCTCACGATTCCACGTTT 247061

QY 917 CTGGCTTTCCTGGTTCCGCCTATAGGATTCAATTCTCATGATGTTCACTGGTGGAGGG 976
 DB 247060 ATAACTAAATTAGTCATACTTGTGCTTGGTGGAGGG 247001

QY 977 GGATGACCCACTCCGAGTGGTATTGGAAAGATCATTTTCATGATTGGATTGCTTTT 1036
 DB 247000 CG----CCCACCCGGTTATCAGAGAGACTCTGGATTGATCTCTTACTGTTT 246946

QY 1037 ATTGGTTTCTCATGGTTGATGGATTCTAGGATTCTAGGATTCTAGGATTCTAG 1095
 DB 246945 GTTCATGGC---TGACTATGATTCTCTCTGAAATCTGACCTCTGACAGACACA 246889

QY 1096 AAATTACAGATTATTGGATATGGATTGGACTCTA 1151
 DB 246888 AAATTACAGATTCTGCGATTGCTGACTCTATATGGACTCTA 246829

QY 1152 ACCAGATAATACCC-----TATGCTTAATGTAACAGCAAAAGCTCTGCAAGACTAT 1206
 DB 246828 AAGCTGAAAATCCCGATCTGTCAGTGTAAAGGGTCTAAGGGTTG 246769

QY 1207 TCTGRATTTCATTTCCTGGATTACTGAAATAGTACAGATGTGGAA---TTTATTGTT 1263
 DB 246768 CCTG--TTAGTGTTCCTGCTGNTACAGCATGGCTGAGATGGTTTTTTTCT 246711

QY 1264 TTAGTTTAAGACTCTGCAACGGCTCTAGGATAGAAACCTTAAGTCTGACTTC 1323
 DB 246710 TTGTTTTGAAAGCAAGCTTAATGGCTCTGAAAGTTGAAACCTGGAAAGTCTGACTTC 246651

QY 1324 AATCAAACGGTAGTGTGATACTGCAAAAGACTGTATACTGCAAAAGACTGTATACT 1366
 DB 246650 AGT---GGTATAGTGTGAACTGCAAGATGTATACTGTTGAGTACATTGTTAT 246595

QY 1367 TTAATATATTGATTATTGTTATTGTTCTGGATTAGTTGTTGGTTCTGTGAA 1426
 DB 246594 TAATATACTTTAACAAATTAACTTGTAAATTGTTGTTGTTCTCTAA 246535

QY 1427 AAAACTTGGATTTTTTCTGTAATCTGGPATTANGTTCTCTTAAATAAGGTTATG 1486
 DB 246534 GGTAATCTGGATTATTGTTCTGTTCTCTTACCCATAAGGTAACA 246476

QY 1487 ANTGGCTGCCAACATTGACTGTTGACTACATGACATGACTCTCT---CA 1542
 DB 246415 AATGCTTGTGCTCAAAAGTCCCTTAACTCGAACCTAACCCATGCTCTGCGCC 246416

QY 1543 AAAAAAAGATGCTTCATAGTTGTTATTGTATATGAAAGAGTCATAATTTC 1602
 DB 246415 CCTAAACGAAATGTCCTAGTGTATTAAATATGAAAGTCATAATTTC 246356

QY 1603 AAGTATATTGTTCTGAAAGAAATGATCATATAATCTGAAAGAAAAGTTGCTTAC 1662
 DB 246355 AATATATATTCTCAATGGAAAAGATCAT-ALTCGAAAGAGTTATTAC 246297

QY 1663 CCAAAATCTAATGCTTAATCCGCTTCACTCCCTCCAGGGAAATC 1722
 DB 246256 CCCAACCTAA-TGGTCAAGGCCAACCTGGCAAAACACTCCCTCTGGGGAAATC 246239

QY 1723 TTAATCTTATGCTCAACTTAATAAATGATGATAAACACTTTTAAATAAACC 1782
 DB 246238 GAATACTCTATGGCTCACCTTAACATGACTTAAATGACTTAAACCCA 246179

QY 1783 TAAGGTTTCTTCTGCTGAGCATGACCACTTATAACTGGGGTGGGGATGCTGTT 1842
 DB 246178 TAAGG-ATATTTCCTCCTCACATGACCACTTAACTGAGATAGTATGCGCTT 246121

QY 1843 GTTTCTAATTATACPIATTTCAGCTCTGTTGATTGAAATCATCTGGTTTTG 1902
 DB 246120 ATTTTAATTGATCTATTCTGTTGAAATATCATCTGGTTTTG 246061

QY 1903 CCTTAACCTCTTAAATGTTATAATTCAAAATCC 1962
 DB 246060 CCTTAATCCCTAACTGTTATATTAATCCAGATACTCC 246001

QY 1953 ATACTAATATTGATGCAATTCTGTTAGGTTATGTTCAATCTGGTTTTG 2017
 DB 246000 ATAACTAAATTAGTCATACTTGTGCTTGGTGGAGGG 245941

Result No.	Score	Query	Match	Length	DB ID	Description	Summaries
1	2065	100.0	3091	11	BC050026	mRNA LOCUS Homo sapiens, cerebellin precursor-like 1, clone IMAGE:4820943, DEFINITION mRNA	RESULT 1 AUTHORS BC050026 TITLE BC050026 JOURNAL BC050026.1 GI:2947708 KEYWORDS HTC. SOURCE Homo sapiens (human) ORGANISM Homo sapiens REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. COMMENT NIH-MG Project URL: http://ngc.nci.nih.gov Contact: MG help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. Tissue Preparation: Michael J. Brownstein (NHGRI) & Shiraki CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LILN) DNA Sequencing by: Baylor College of Medicine Human Genome
2	1077	52.2	2405	11	AK032406	B050026 LOCUS Homo sapiens, cerebellin precursor-like 1, clone IMAGE:4820943, DEFINITION mRNA	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
3	1012.8	49.0	2802	11	AK032621	Mus muscu	JOURNAL BC050026.1 GI:2947708 KEYWORDS HTC. SOURCE Homo sapiens (human) ORGANISM Homo sapiens REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. COMMENT NIH-MG Project URL: http://ngc.nci.nih.gov Contact: MG help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. Tissue Preparation: Michael J. Brownstein (NHGRI) & Shiraki CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LILN) DNA Sequencing by: Baylor College of Medicine Human Genome
4	751	36.4	905	12	BI668562	603293849	RESULTS

SEQUENCING CENTER						
Center code: BCM-HGSC						
Web site: http://www.hgsc.bcm.tmc.edu/cdna/						
Contact: amg@bcm.tmc.edu						
Series:	IRAX	Plate:	71	Row:	C	Column:
This clone has the following problem: retained intron.						
FEATURES	Location/Qualifiers					
source						
1..3091	/organism="Homo sapiens"					
/mol type="mRNA"						
/db_xref="taxon:9606"						
/clone IMAGE:4B2943"						
/tissue type="Brain, hippocampus"						
/clone Lib="NIH_MCC_95"						
/lab host="DH10B"						
/not=vector: pBluescript"						
RIGIN						
Query Match	100.0%	Score: 2055;	DB 11;	Length: 3091;		
Best Local Similarity	100.0%	Pred. No.: 0;				
Matches 2065;	Conservative	0;	Mismatches	0;	Indels	0;
968	GTGAAATGTAGGGCTTGATGACTTTCAGATGTCAGAGAACGAGTGGGTGCAGGGGCC	60				
61	CAGCAGGGCTGATTCTGGCGGGAGTAGGTAANGGTCTGCAAGCTGAGGAGCTGGGAGA	120				
1028	CAGCAGGGCTGATTCTGGCGGGAGTAGGTAANGGTCTGAGGAGCTGGGAGA	108				
121	AAAGACACAGGTTACAGACCGGGAGAGCTGGGGAGA	180				
1088	AAAGACACAGGTTACAGACCGGGAGAGCTGGGGAGA	114				
181	CAGAATTGGCTGAATCTGGCGGGAGACCGGGATCCGGGTAGAGGCACGCTGACCTA	240				
1148	CAGATTGGTGGAACTGGCCACGGGTCTGGGGAGCTGGGGAGCTGGGGAGCTGGGGAG	120				
241	GCCGCTAGCATCTGCCGAGCACCGGGATCCGGGTAGAGGCACGGGGAGCACC	300				
1208	GCCGGTAGCATCTCCGAGACCGGGATCCGGGTAGAGGCACGGGGAGCTGGGGAG	126				
301	AGCCGCAAGGGCTCCGGCTGGCCACGGGTCACTGGGGAGCTGGGGAGCTGGGGAG	360				
1268	AGCCGCAAGGGCTCCGGCTGGCCACGGGTCACTGGGGAGCTGGGGAGCTGGGGAG	132				
361	TCCGGGGTGGGGCTGGGGAGCTGGGGAGCTGGGGAGCTGGGGAGCTGGGGAG	420				
1328	TCCGGGGTGGGGAGCTGGGGAGCTGGGGAGCTGGGGAGCTGGGGAGCTGGGGAG	138				
421	AACGGACCGAGCCATGGGGCAAGTGTGGGGCTGGGGAGCTGGGGAGCTGGGGAG	480				
1388	AACGGACCGAGCCATGGGGAGCTGGGGAGCTGGGGAGCTGGGGAGCTGGGGAG	144				
481	GCCACGGGACTCCAAAGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	540				
1448	GCCACGGGACTCCAAAGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	150				
541	TCCAAGGTGGCTTCGGGGAGCTGGAGACCAAACAGACGGCAATCGAGAAC	600				
1508	TCCGGGTGGCTTCGGGGAGCTGGAGACCAAACAGACGGCAATCGAGAAC	156				
601	AAGACGGCAGTCATTACTCTGATAGATCTGGTGAATGTTTCACATTTTCACAT	660				
1568	AAGACGGCAGTCATTACTCTGATAGATCTGGTGAATGTTTCACATTTTCACAT	162				
661	GACGGCTGCTCTTGGCTTCAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAA	723				

Db	2708	CCTTAATTAATGATTGATAATAACCCACTTATTAAACCACTAAGGTTCCTTTTC 2767	JOURNAL REFERENCE	Nature 420, 563-573 (2002)
OY	1801	CGTAGACATGACCACCTTATTAACTTACGGGGATGGCTGTTCTCAATTACCAT 1860	AUTHORS	6 (bases 1 to 2406) Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirozane,T., Hiraoka,T., Hori,F., Imotani,K., Itoii,Y., Kasuga,I., Kondo,S., Koono,H., Konda,M., Kato,T., Kawai,J., Koijima,Y., Kondo,S., Koono,H., Konda,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Nakamura,C., Kurihara,C., Miyazaki,A., Murata,M., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shiba,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takanaka,T., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
Db	2768	CGTAGACATGACCACCTTATTAACTTACGGGGATGGCTGTTCTCAATTACCAT 2827	JOURNAL REFERENCE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome.resgsc.riken.go.jp/ URL:http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
OY	1861	TTCAGAACGCTCTGTTGATTGAAAGTACATCTGGTTGCCTAACCTCTTAATG 1920	JOURNAL REFERENCE	Fax: 81-45-503-9216)
Db	2828	TTCAGAACGCTCTGTTGATTGAAAGTACATCTGGTTGCCTAACCTCTTAATG 2887	JOURNAL REFERENCE	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
OY	1921	TATATATTATCCTGTTACTAATTATTAATTAAATCCATATCTAAATTAGTCGA 1980	JOURNAL REFERENCE	Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/
Db	2888	TATATATTATCCTGTTACTAATTATTAATTAAATCCCATATCTAAATTAGTCGA 2947	JOURNAL REFERENCE	URL:http://fantom.gsc.riken.go.jp/
OY	1981	ATATCTGCTTGTAGGTCTATGAAATTATGCTGTATAGAA 2040	JOURNAL REFERENCE	1 . 2406 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:6430538G21" /db_xref="NCI:2395903" /db_xref="TAXON:10090" /clone="6430538G21" /sex="male" /tissue_type="olfactory brain" /clone_id= RIKEN full-length enriched mouse cDNA library"
Db	2948	ATATCTGCTTGTAGGTCTATGAAATTATGCTGTATAGAA 3007	JOURNAL REFERENCE	673 . 1269 /dev_stage="adult" /note="unnamed protein product; CEREBELLIN-LIKE GLYCOPROTEIN PRECURSOR (SWISSPROT Q9NUT7, evidence: FASTY, 96%ID, 100%length, match=394) putative" /protein_id="BAC27855_1" /protein_id="GI:26328229" /translaton="MGRARRSSSPGLISTRAANSKVAFARSTNHPEPEMSNKTRITYDQILNVNGNF PATDSRKSSSSPLGISTRAANSKVAFARSTNHPEPEMSNKTRITYDQILNVNGNF FILESVPVATRKGIVSYSEHVIKVYQSOITIONQNMCKPVISAFAGDKDVTFREAAATN GVYLKDQYKLVLDKEKGNLGGWQTSFSGFLVEFL"
OY	2041	TAAGATTAATATAATGTTAAAAAAA 2065	JOURNAL REFERENCE	CDS /note="putative"
Db	3008	TAAGATTAATATAATGTTAAAAAAA 3032	JOURNAL REFERENCE	/codon_start=1 /protein_id="BAC27855_1" /protein_id="GI:26328229" /translaton="MGRARRSSSPGLISTRAANSKVAFARSTNHPEPEMSNKTRITYDQILNVNGNF PATDSRKSSSSPLGISTRAANSKVAFARSTNHPEPEMSNKTRITYDQILNVNGNF FILESVPVATRKGIVSYSEHVIKVYQSOITIONQNMCKPVISAFAGDKDVTFREAAATN GVYLKDQYKLVLDKEKGNLGGWQTSFSGFLVEFL"
RESULT	2		JOURNAL REFERENCE	polyA_signal polyA_site ORIGIN
AK032406			JOURNAL REFERENCE	Query Match 52.2%; Score 1077; DB 11; Length 2406; Best Local Similarity 77.0%; Pred. No. 6.5e-183; Matches 1624; Conservative 0; Mismatches 395; Indels 90; Gaps 22;
LOCUS	AK032406	Mus musculus adult male olfactory brain cDNA, RIKEN full-length	JOURNAL REFERENCE	
DEFINITION			JOURNAL REFERENCE	
		HTC 18-SEP-2003	JOURNAL REFERENCE	
enriched library. Clone: 6430538G21 Product: CEREBELLIN-LIKE			JOURNAL REFERENCE	
GLYCOPROTEIN PRECURSOR, full insert sequence.			JOURNAL REFERENCE	
AK032406			JOURNAL REFERENCE	
VERSION	AK032406.1	GI:26328228	JOURNAL REFERENCE	
KEYWORDS		HTC ; CAP trapper.	JOURNAL REFERENCE	
SOURCE		Mus musculus (house mouse)	JOURNAL REFERENCE	
ORGANISM		Mus musculus	JOURNAL REFERENCE	
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			JOURNAL REFERENCE	
1			JOURNAL REFERENCE	
Carninci,P. and Hayashizaki,Y.			JOURNAL REFERENCE	
High-efficiency full-length cDNA cloning			JOURNAL REFERENCE	
Meth. Enzymol. 303, 19-44 (1999)			JOURNAL REFERENCE	
99279253			JOURNAL REFERENCE	
10349636			JOURNAL REFERENCE	
			JOURNAL REFERENCE	
2			JOURNAL REFERENCE	
Itoh,M., Konno,H., Oizaki,Y., Muramatsu,M. and Hayashizaki,Y.			JOURNAL REFERENCE	
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			JOURNAL REFERENCE	
Genome Res. 10 (10), 1617-1630 (2000)			JOURNAL REFERENCE	
20499374			JOURNAL REFERENCE	
11042159			JOURNAL REFERENCE	
3			JOURNAL REFERENCE	
Shibata,K., Itoh,M., Aizawa,K., NagaoKA,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Itoii,Y., Nakamura,S., Hazama,M., Nishime,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.			JOURNAL REFERENCE	
RIKEN integrated sequence analysis (RISA) system--84-format sequencing pipeline with 384 multicapillary sequencer			JOURNAL REFERENCE	
Genome Res. 10 (11), 1757-1771 (2000)			JOURNAL REFERENCE	
20530913			JOURNAL REFERENCE	
11076861			JOURNAL REFERENCE	
4			JOURNAL REFERENCE	
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			JOURNAL REFERENCE	
Functional annotation of a full-length mouse cDNA collection			JOURNAL REFERENCE	
Nature 409, 685-690 (2001)			JOURNAL REFERENCE	
5			JOURNAL REFERENCE	
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.			JOURNAL REFERENCE	
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			JOURNAL REFERENCE	
6			JOURNAL REFERENCE	
CCAGGCCAAACTGATTGGGGGGGAG-GAGTAGGTAGGGTCTGGCTCTGATGAGCTCT 454			JOURNAL REFERENCE	

SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	Carninci, P., and Hayashizaki, Y. High-efficiency full-length cDNA cloning. J. Mol. Biol. 292:7253-7262 (1999).
AUTHORS	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	1049374
PUBMED	11042159
REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishime, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiiwara, S., Inoue, K., Tagawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsubara, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashizaki, Y., Hayatsu, N., Hirakawa, K., Hirczane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komio, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnishi, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasai, D., Shibusawa, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22, Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp; URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22, Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp; URL: http://genome.gsc.riken.go.jp/
COMMENT	CDNA library was prepared and sequenced in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.
FEATURES	source

Db	241	AGAAGAAAGATAGATCATATAATCTGACAGGGAAAAGTGTCTACCCAAAATCTAAGTGC	300	Best Local Similarity 100.0%; Pred. No. 1.9e-98; Matches 606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1678	TCAATCCCTGAGGCTCAGAAAAACAGCTCCCCCTCGAGGGAAACTTACATTATTGCT	1737	Qy 337 ATGGCTCGGGCGCGGGGCGCTGCTGGCTCTCACGCTG 396
Db	301	TCAATCCCTGAGGCTCAGAAAAACAGCTCCCCCTCGAGGGAAACTTACATTATTGCT	360	Db 1 ATGGCTCGGGCGCGGGGCGCTGCTGGCTCTCACGCTG 60
Qy	1738	CAACTTTAATTAATATGATTGATAATACCACTTATTAACCTAAGGTTTTTTT	1797	Qy 397 CCGGGGTCGCCCTGTGGCACAGAACACAGGCCATGTGCTGGAGGCAAGTGT 456
Db	361	CAACTTTAATTAATATGATTGATAATACCACTTATTAACCTAAGGTTTTTTT	420	Db 61 CCGGGGTCGCCCTGTGGCACAGAACACAGGCCATGTGCTGGAGGCAAGTGT 120
Qy	1798	TTCGGTAGACATGACCACCTTATAACTGGTGGGATGCTGTCTAATTATACC	1857	Qy 457 CTGGGGTGCGGACTCTAACCGGGCTCTCCCGCTGCTGGAGGCAACGGACCCATGTGCTGGAGGCAAGTGT 516
Db	421	TTCGGTAGACATGACCACCTTATAACTGGTGGGATGCTGTCTAATTATACC	480	Db 121 CTGGGGTGCGGACTCTAACCGGGCTCTCCCGCTGCTGGAGGCAACGGACCCATGTGCTGGAGGCAAGTGT 180
Qy	1858	TATTTTCAAGGCTCTGCTGCTGATTGAGTATCATCTGTTTGCCCTAACCTTAA	1917	Qy 517 GGATATGGCTGGGCGGCCAACCTCAAGGCTGGGCGCAACAC 576
Db	481	TATTTTCAAGGCTCTGCTGCTGATTGAGTATCATCTGTTTGCCCTAACCTTAA	540	Db 181 GGATATGGCTGGGCGGCCAACCTCAAGGCTGGGCGCAACAC 240
Qy	1918	TGTGATATTTATCTGTTAGTAACTAAATTAACTCCATATCTAAATTGT	1977	Qy 577 CAGAGCCATCCAGATGGCACAAAGAGGCCATCTTACTTCGATCAGTCCTGTTG 636
Db	541	TGTGATATTTATCTGTTAGTAACTAAATTAACTCCATATCTAAATTGT	600	Db 241 CAGAGCCATCCAGATGGCACAAAGAGGCCATCTTACTTCGATCAGTCCTGTTG 300
Qy	1978	GCAATATCTGCTCTTGTATAGGGCTATAGTAAATTCAATGAATTCTGTTATA	2037	Qy 637 AATGGGTAATTTTTCAATTGGAGCTGTCTTGTAGACCAAGAAAGGATTAC 696
Db	601	GCAATATCTGCTCTTGTATAGGGCTATAGTAAATTCAATGAATTCTGTTATA	660	Db 301 AATGGGTAATTTTTCAATGGAGCTGTCTTGTAGACCAAGAAAGGATTAC 360
Qy	2038	GAATAAGGATTATAATGTAAAGA	2065	Qy 697 AGTTCACTTTCAGGATTAAAGTCTTACCAAGGCCAAACTATCCAGGTTAACCTGATG 756
Db	661	GAATAAGGATTATAATGTAAAGA	688	Db 361 AGTTCACTTTCAGGATTAAAGTCTTACCAAGGCCAAACTATCCAGGTTAACCTGATG 420
RESULT	6			Qy 757 TAAATGGAAAACGAAATACTGCTTTCGGGGACAAGAGTTACTCTGGAAAGCT 816
AY418431				Db 421 TTATGGAAAACGAAATACTGCTTTCGGGGACAAGAGTTACTCTGGAAAGCT 480
LOCUS				Qy 817 GCCAGATGGTGTCTGCTACTGATAAGAGGATAAGGTCTTACCTAAACCTGAG 876
DEFINITION				Db 481 GCCRAGATGGTGTCTGCTACTGATAAGGTCTTACCTAAACCTGAG 540
Homo sapiens CBLNL1 gene, partial sequence,				Qy 877 AAAGCTAAATTGGTGTCTGCTACTGATAAGAGGATAAGGTCTTACCTAAACCTGAG 936
genomic survey sequence.				Db 541 AAAGCTAAATTGGTGTCTGCTACTGATAAGGTCTTACCTAAACCTGAG 600
AY418431				Qy 937 CTATAG 942
ACCESSION				Db 601 CTATAG 606
AY418431.1				
VERSION				
KEYWORDS				
SOURCE				
Homo sapiens (human)				
ORGANISM				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 606)				
REFERENCE				
Clark, A.G., Gianiowski, S., Nielsen, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
AUTHORS				
TITLE				RESULT 7
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				AY418432
JOURNAL				LOCUS
Science 302 (5652), 1960-1963 (2003)				AY418432
PUBLISHED				DEFINITION
14671302				Pan troglodytes CBLNL1 gene, VIRTUAL TRANSCRIPT, partial sequence, Genomic survey sequence.
REFERENCE				AY418432
Clark, A.G., Gianiowski, S., Nielsen, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				ACCESSION
FEATURES				AY418432.1 GI:39774392
source				KEYWORDS
1. 606				SS.
JOURNAL				SOURCE
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				Pan troglodytes
COMMENT				Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
These sequences were made by sequencing genomic exons and ordering them based on alignment.				These bases 1 to 606.
FEATURES				Clark, A.G., Gianiowski, S., Nielsen, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
source				Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL				Science 302 (5652), 1960-1963 (2003)
PUBLISHED				PUBLISHED
14671302				2 bases 1 to 606.
REFERENCE				Clark, A.G., Gianiowski, S., Nielsen, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Authors				Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
Query Match				Science 302 (5652), 1960-1963 (2003)
ORIGIN				PUBMED
29.3%; Score 606; DB 29; Length 606;				14671302
gene				
gene				
/organism="Homo sapiens"				
/mol_type="genomic DNA"				
<1. . >606				
/db_xref="taxon:9606"				
/gene="CBLNL1"				
/locus_tag="HCM6555"				

Query Match	Match Similarity	Score	DB 1.2;	Length	700;	FEATURES	source
QY	Best Local Similarity 96.1% ; Matches 544; Conservative 0 ; Mismatches 21; Indels 1; Gaps 1;	25.2%	Score 520.4; DB 1.2;	Length 700;		Seq primer: -40m13 fwd. BT from Amersham High quality sequence stop: 431.	
Db	5 1168 GCTTAATGAAAGTCAAAGTGTCTCGCAAGACTTATTCTGAATTTCATTCCCTGGAA 1227	1. .504	Location/Qualifiers				
QY	1228 TTACTGAATTAGTTACAGATGTGCAATTTTATGTTAAGACTGCCAACCA 1287		/organism="Homo sapiens"				
Db	65 TTACTGAATTACAGTCAAAGCTGTCTCGCAAGCTTATTCTGCCTGGAA 64		/mol_type="mRNA"				
QY	1288 GGTCDAAGGATTGAAACTCTAAAGTCTGACTCATCAACGGTTGTGATACTGC 1347		/db_xref="NCBI IMAGE:1408691"				
Db	125 GGCTTAAGGATTGAAACTCTAAAGTCTGACTCATCAACGGTTGTGATACTGC 184		/sex="male"				
QY	1348 CAAGAACCTGTATACTGTGTTAATAATGTTATTGTTCTTGAAATTA 1407		/lab_host="DH10B"				
QY	185 CAAGAACCTGTATACTGTGTT-ATATATGTTATGTTCTTGAAATTA 243		/clone_lib="Soares testis NHT"				
Db	1408 GTTGTTGTTGTTCTGTTGAAAAAACTCTAAAGTCTGACTCATCAACGGTTGTGATACTGC 1467		/note="Vector: pRTID-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dR) primer [5]. TGTACCAATTGAACTGGAGCGGCCAATTTTTTTTTTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library went through one round of normalization to C05, and was constructed by Bento Soares and M. Fatima Bonaldo."				
ORIGIN							
QY	1468 CTCTTAATAATAAGTTAATAATGTTGACAGATACTCG 1527	24.4%	Score 504; DB 9;	Length 504;			
Db	304 CTCTTAATAATAAGTTAATAATGTTGACAGATACTCG 363	10.0%	Best Local Similarity 10.0% ; Pred. No. 3.8e-80;				
QY	1528 ACATGACTCTCTCAAAAAAAAGATGCTCATAGTGTATTAAATGTTGAA 1587	0	Matches 504; Conservative 0; Mismatches 0;				
Db	364 ACATGACTCTCTCAAAAAAAAGATGCTCATAGTGTATTAAATGTTGAA 423	0	Indels 0; Gaps 0;				
QY	1588 AGACTCATATACTTCTCAAGTTATTTCTAAAGAAAGTATGCTATAATCTGACAG 1647						
Db	424 AGACTCATATACTTCTCAAAAAAAAGATGCTCATAGTGTATTAAATGTTGAA 483						
QY	1648 GAAAAGTGTCTTACCCAAAATCTAAGTGTCAATCCCTGAGCCTCAGGAAACAGCTC 1707						
Db	484 GAAAAGTGTCTTACCCAAAATCTAAGTGTCAATCCCTGAGCCTCAGGAAACAGCTC 543						
QY	1708 CCTCGAGGAAATCTTACTTAT 1733						
Db	544 CCCCTCTCGAAGGGAAAATCTTAAAT 569						
RESULT	11 AA868507	504	bp	mRNA	linear EST 04-JUN-1999	RESULT 12	DNA
LOCUS	ak43b06	51	Soares_testis_NHT	Homo sapiens	cDNA clone IMAGE:1408691	AY418433	linear GSS 17-DEC-2003
DEFINITION	3 ' mRNA sequence.						
ACCESSION	AA868507						
VERSION	AA868507.1						
KEYWORDS	EST.						
SOURCE	Homo sapiens (human)						
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 (bases 1 to 504)						
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.						
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index						
JOURNAL	Unpublished (1997)						
COMMENT	Contact: Robert Straussberg, Ph.D.						
CDNA Library Preparation:	M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.						
CDNA Library Arrayed by:	Greg Lennon, Ph.D.						
DNA Sequencing by:	Washington University Genome Sequencing Center						
Clone distribution:	NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LINN at: www.bio.llnl.gov/bbrp/Image/image.html						
Insert Length:	667 Std Error: 0.00						

AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
JOURNAL Biopol. 12 (22), 1965-1969 (2002)
MEDLINE 2235534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 0161 200830
 Fax: 0161 2360409
 Email: Simon.Hubbard@umist.ac.uk.
FEATURES Location,Qualifiers
 source
 1..750
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="CHEST6801"
 /dev_stage="36"
 /lab_host="DEHOB"
 /clone_lib="CSEQCHN75"
 /note="Organ: trunks; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adaptors, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 19.2%; Score 396; DB 13; Length 750;
 Best Local Similarity 76.5%; Pred. No. 8.8e-61;
 Matches 578; Conservative 0; Mismatches 165; Indels 13; Gaps 7;
 Qy 572 CCAACCACCGAGCCATCCGGAGATGAGCAAAAGAGGCCATCAATTACTTCGATCAGATCC
 Db 1 CCAACCACCGAGCCATCCGGAGATGAGCAAAAGAGGCCATCAATTACTTCGATCAGATCC 631
 Qy 632 TGGTGAATGTGGTAATTTTTCATGGTGAATCTGAGTCTGTCTTGAGCAAGAAAGGAA 691
 Db 61 TAGTAAACCTGGGAATTTTTCAGTGGAAATCTGAGTGAATCTGCTTGTGTCAGAAGAA 120
 Qy 692 TTACAGTTTCAAGTTTCACTGATTAAGTCTACCAAGCCAACACTTCCAGGTTAAC 751
 Db 121 TTACAGTTTCACTGATTAAGTCTACCAAGCCAACACTTCCAGGTTAAC 180
 Qy 752 TGATGTAAATGGAAAAACCGTAATACTCGCCTTGCGGGGACAACATTTACTCTG 811
 Db 181 TGATGTCAATGGAAAGGAGTCATCTGCTTGTGCGGGACAACAGCTCACTGTG 240
 Qy 812 AAGCTGCCACGAATGGTGCCTGCTCACTTAGATAAGGAGTAAGTTTACCTAAAC 871
 Db 241 AAGCTGCCACTAAGGATGCCCTGCTCACTAGCAAGGAGTAAGTTTACCTGAGC 300
 Qy 872 TGGAGAAAGGTAATTGGTGGGGCTGGAGTCCAGTATTCCAGTTTCCTGCTGTG 931
 Db 301 TGGAGAAAGGTAATCTGGTGGGGATGCCAGTATTCACTGCTTCTGGCTTCTGCT 360
 Qy 932 TCCGCCCTATGGATTCAATTCTCCATGTCATGTCATGCCACTCT 991
 Db 361 TCCCCCTGTA-AGTCATTTCTGCTGATGTCAGTGTGGAGTCATGGCT 419
 Qy 992 GAGTTATGGAAGATCATTTTCATCATTTGATTGATGTCCT-TTATGGTTCTCATG 1050

Search completed: May 15, 2004, 06:48:05
 Job time : 5405 secs

Db 420 CTGTCATGAGATACTCCGTCATGTGGGATGATGTTCCATTGTTTCAG 479
 Qy 1051 GGTGGATATGGATTC---TAAGGATTCTAGCCGCTGCTGACAAATCACAAATTTCACAG 1106
 Db 480 GGGAATATAGATTCCTGATGGATTTGCCCATCTGAACTACAGAGTTCA 539
 Qy 1107 ATTATTTGTTGCTGTCGTTCAAGATAATTGGATGGGACTCA--AGAGATAATACC 1164
 Db 540 GAATTCGTTGTTTAAATACATAATTTGGATGAGCTTAAGCAGGATAATAA 598
 Qy 1165 TATGCTTAATGTAACGTTAAAGCTGTGCAAGACTTATCTGAATTTCATTTCTCG 1224
 Db 599 CTGCTTAAAGTACGGTTAAAGCTGCTGAGGGTTATCG-GTATGATACTG 657
 Qy 1225 GGATTAATGAAATTGATTCAGATGTTGGAAATTTTATTGGTTAGTTAAAGACTGGCAA 1284
 Db 658 GGACTTATGATTGATCTGAGAACTGAACTGAACTGAACTGAACTGAACTG 714
 Qy 1285 CCAGGTCTAGGATAGAAAACCTTAAGCTTCTGCTGAGGGTTATCG 1320
 Db 715 CCAGGTCTATAATTAAGCCGAAATTGAGTTGAGTTGAGTTGAGAC 750